

APPENDIX A
CLEAN VERSION OF SUBSTITUTE SEQUENCE LISTING
(Application Serial No. 10/046,671)



SEQUENCE LISTING

<110> Boot, Hendrik J.
Huurne ter, Anna A.H.M
Peeters, Bernardus P.H.

<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671

<141> 2002-01-14

<150> PCT/NL00/00493

<151> 2000-07-13

<150> EP 99202316.8

<151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

<210> 1

<211> 6

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: KpnI restriction site

<400> 1

ggtaac

6

<210> 2

<211> 16

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<223> Primer ANC1

<400> 2

ggggacccgc gaacgg

16

<210> 3

<211> 18

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<223> Primer RTAM
 <400> 3
 aattggtgtc cacacctg 18

 <210> 4
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer RTAP

 <400> 4
 atacaggacc taactggg 18

 <210> 5
 <211> 30
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer HY3P

 <400> 5
 aacgttttcc tcacaatccg cgggactggg 30

 <210> 6
 <211> 22
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer AGTM

 <400> 6
 gagactccca ggtacctcac tc 22

 <210> 7
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer AC3

 <400> 7

ggtagccaca tgtgacag	18
<p><210> 8 <211> 21 <212> DNA <213> Infectious bursal disease virus</p>	
<p><220> <221> misc_feature <223> Primer HY3MR</p>	
<400> 8 ccagtcccgc ggattgtgag g	21
<p><210> 9 <211> 17 <212> DNA <213> Infectious bursal disease virus</p>	
<p><220> <221> misc_feature <223> Primer M13F-17</p>	
<400> 9 gtaaaacgac ggccagt	17
<p><210> 10 <211> 18 <212> DNA <213> Infectious bursal disease virus</p>	
<p><220> <221> misc_feature <223> Primer AC4</p>	
<400> 10 accagccaa tcacatcc	18
<p><210> 11 <211> 19 <212> DNA <213> Infectious bursal disease virus</p>	
<p><220> <221> misc_feature <223> Primer AC9</p>	
<400> 11 ctcaaagaag atggagacc	19

<210> 12
 <211> 24
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer M13F-24

 <400> 12
 cgccaggggtt ttcccagtca cgac 24

 <210> 13
 <211> 22
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer AC5

 <400> 13
 aaggccttca tggaggtggc cg 22

 <210> 14
 <211> 21
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer AGTP

 <400> 14
 cttgagtgag gtacctggga g 21

 <210> 15
 <211> 21
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer vvVP3CM

 <400> 15
 gagaaaattt cgcattccgat g 21

 <210> 16
 <211> 22
 <212> DNA

<213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer M13R
 <400> 16
 tcacacagga aacagctatg ac 22
 <210> 17
 <211> 30
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer ATG3
 <400> 17
 catcgctgcg atcgtttgtc tgatctctac 30
 <210> 18
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer
 <400> 18
 atccgggccc taaggagg 18
 <210> 19
 <211> 17
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer ANC4"
 <400> 19
 gccaaagtcgg tgtgcag 17
 <210> 20
 <211> 21
 <212> DNA
 <213> Infectious bursal disease virus
 <220>

```

<221> misc_feature
<223>Primer HY0P

<400> 20
tatcattgat ggtcagtaga g                                21

<210> 21
<211> 17
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer HY2M

<400> 21
caccggcaca gctatcc                                17

<210> 22
<211> 26
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer T7EcoRI

<400> 22
ggaattctaa tacgactcac tatagg                        26

<210> 23
<211> 21
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer HY3M

<400> 23
ccagtcccgc ggattgtgag g                                21

<210> 24
<211> 17
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer M13F

```

<400> 24
 gtaaaacgac ggccagt 17

<210> 25
 <211> 16
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer HY4M

<400> 25
 ccggcacagc tadcct 16

<210> 26
 <211> 17
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer ANC2

<400> 26
 ctgcctgtcc tggagcc 17

<210> 27
 <211> 20
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer HY4P

<400> 27
 acataatccg ggccataagg 20

<210> 28
 <211> 17
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer ANC3

<400> 28
 cgatgggcgt tcgggtc 17

<210> 29
<211> 18
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer ANC5

<400> 29
cccatctgga gcatatcc

18

<210> 30
<211> 18
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer AC6

<400> 30
ttcacctggg gtactccg

18

<210> 31
<211> 30
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> primer_bind
<222> (1)..(30)
<223> Anchor

<400> 31
cacgaattca ctatcgattc tggatccttc

30

<210> 32
<211> 20
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> primer_bind
<222> (1)..(20)
<223> Anchor primer

<400> 32
gaaggatcca gaatcgatag

20

<210> 33
 <211> 19
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(19)
 <223>Primer ANC0

 <400> 33
 ggggacccgc gaacggatc 19

 <210> 34
 <211> 16
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(16)
 <223> Primer ANC1

 <400> 34
 ggggacccgc gaacgg 16

 <210> 35
 <211> 47
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(47)
 <223> Primer T7AC0

 <400> 35
 ggaattctaa tacgactcac tataggatac gatcgggtctg accccgg 47

 <210> 36
 <211> 15
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(15)
 <223> Primer BNC1

 <400> 36

ggggggccccc gcagg 15

<210> 37
<211> 45
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> primer_bind
<222> (1)..(45)
<223> Primer T7BC1"

<400> 37

ggaattctaa tacgactcac tataggatac gatgggtctg accct 45

<210> 38
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> 5'-Terminus of the A-segment coding strand
of IBDV

<400> 38
ugauacgauc 10

<210> 39
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> 5'-Terminus of the A-segment coding strand
of IBDV

<400> 39
agauacgauc 10

<210> 40
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>

<221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the A-segment coding strand
 of IBDV

 <400> 40
 ggauacgauc 10

<210> 41
 <211> 10
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> Consensus sequence corresponding to the
 5'-terminus of the A-segment coding strand of
 IBDV

<400> 41
 ggauacgauc 10

<210> 42
 <211> 4
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(4)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 42
 cggg 4

<210> 43
 <211> 8
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 43
 cggguccc 8

<210> 44
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 44
cgggucccu

9

<210> 45
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 45
cggguccccc

9

<210> 46
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 46
cggguccccc c

11

<210> 47
<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 47
cggguccccc cu 12

<210> 48
<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 48
cggguccccc cc 12

<210> 49
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Consensus complementary sequence of the
5'-terminus of the A-segment non-coding strand of
IBDV

<400> 49
cggguccccc 9

<210> 50
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> 5'-Terminus of the B-segment coding strand
of IBDV

<400> 50
ugauacgaug 10

<210> 51
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the B-segment coding strand
 of IBDV

<400> 51
 ggauacgaug 10

<210> 52
 <211> 10
 <212> RNA

<213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> Consensus sequence of the 5'-terminus of
 the B-segment coding strand of IBDV

<400> 52
 ggauacgaug 10

<210> 53
 <211> 8
 <212> RNA

<213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
 of the B-segment non-coding strand of IBDV

<400> 53
 gggggcca 8

<210> 54
 <211> 8
 <212> RNA

<213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
 of the B-segment non-coding strand of IBDV

<400> 54
 gggggccu 8

<210> 55
<211> 8
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 55
gggggccc

8

<210> 56
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 56
gggggcccc

9

<210> 57
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 57
gguggcccc

10

<210> 58
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)

<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 58
ggggggccccc c 11

<210> 59
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 59
ggggggccccc g 11

<210> 60
<211> 10
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> Consensus complementary sequence of the
5'-terminus of the B-segment non-coding strand of
IBDV

<400> 60
ggggggccccc 10

<210> 61
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolates D6948, rD6948, UK661
5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,
TKSM and HK46

<400> 61
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser

```

                20                25                30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
      35                40                45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
      50                55                60
Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
      65                70                75                80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85                90                95
Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
      100                105                110
Gly Asp Gln Met Ser Trp Ser
      115

```

```

<210> 62
<211> 119
<212> PRT
<213> Infectious bursal disease virus

```

```

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
      region of VP2 of IBDV isolate 96-B4

```

```

<400> 62
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
  1                5                10                15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
      20                25                30
Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
      35                40                45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
      50                55                60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65                70                75                80
Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
      85                90                95
Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
      100                105                110
Gly Asp Gln Met Ser Trp Ser

```

<210> 63
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 96-C4

<400> 63
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Leu Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu
 35 40 45
 Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 64
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of a IBDV isolate 96-C5

<400> 64
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
 1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 65
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 97-B3

<400> 65
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 66
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>

<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate Zoontjes

<400> 66
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60
Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
65 70 75 80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile
85 90 95
Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110
Gly Asp Gln Met Ser Trp Ser
115

<210> 67
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>

<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate OKYMT

<400> 67

```

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1           5           10           15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
      20           25           30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu
      35           40           45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
      50           55           60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65           70           75           80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85           90           95
Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala
      100          105          110
Gly Asp Gln Met Ser Trp Ser
      115

```

```

<210> 68
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
      region of VP2 of IBDV isolate TKSMT

```

```

<400> 68
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1           5           10           15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
      20           25           30
Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu
      35           40           45
Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr
      50           55           60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65           70           75           80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85           90           95

```

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 69
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate HK46-NT

<400> 69
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 70
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<222> (1)..(3260)
<223> Consensus cDNA sequence of IBDV A-segment

<400> 70

ggatacgate	gggtctgaccc	cggggggagtc	acccgggggac	aggcygwcaa	ggyccttggtc	60
caggatggaa	ctcctccttc	tacaaygcta	tcattgatgg	tyagtagaga	tcagacaaac	120
gatcgacgcg	atgacraacc	tgcaagatca	aacccaacag	attgttccgt	tcatacggag	180
ccttctgatg	ccaacaaccg	gaccggcgtc	cattccggac	gacaccctrg	agaagcacac	240
tctcaggtca	gagacctcga	cctacaattt	gactgtgggg	gacacagggg	cagggctaata	300
tgtctttttc	cctggwttcc	ctgggtcaat	tgtgggtgct	cactacacac	tgcagagcaa	360
tggaactac	aagtctgac	agatgtcct	gactgccag	aacctaccgg	ccagytacaa	420
ctactgcagg	ctagtgaagc	ggagtctcac	agtgaagtc	agcacactyc	ctgggtggcgt	480
ttatgcacta	aayggcacca	taaacgccgt	gaccttccaa	ggaagcctga	gtgaactgac	540
agatgttagc	tacaatgggt	tgatgtctgc	aacagccaac	atcaacgaca	aaatygggaa	600
cgtcctagta	ggggaagggg	tmaccgtcct	cagcttacc	acatcatatg	atcttgggta	660
tgtgagrcty	gggtgaccca	ttcccgwat	agggtctygc	ccaaaaatgg	tagcmacatg	720
tgacagcagt	gacaggccca	gagtctacac	cataactgca	gccgatgatt	accaattctc	780
atcacagtac	caascagggt	gggtaacaat	cacactgttc	tcagcyaaay	tygatgccat	840
cacaagcctc	agcrtygggg	gagarctcgt	gtttcaaaca	agcgtccamg	gccttrtact	900
gggygcayac	atctacctya	taggctttga	tgggacwgcg	gtaatcacca	grgctgtggc	960
cgcaracaat	gggctracgr	ccggcacysa	caaccttwtg	ccattcaatm	ttgtgattcc	1020
aacmarcgag	ataaccacgc	caatcacatc	catcaaaactg	gagatagtg	cctccaaaag	1080
tggtggtcag	gcrggggatc	agatgtcrtg	gtcrgcaagw	gggagcctag	cagtgcagat	1140
ccayggtggc	aactatccag	gggccctccg	tcccgtcacr	ctagtrgcct	acgaaagagt	1200
ggcaacagga	tcygtcggtt	cggctgcyyg	ggtagcaaac	ttcgagctga	tcccaaatcc	1260
tgaactagca	aagaacctgg	tyacagaata	cggccgattt	gacccaggag	ccatgaacta	1320
cacaaaattg	atactgagtg	agagggaccg	tcttggcatc	aagaccgtmt	ggccaacaag	1380
ggagtacact	gactttcgys	artacttcat	ggaggtggcc	gacctcaact	ctcccttgaa	1440
gattgcagga	gcattygggt	tcaaagacat	aatccggggc	mtaaggagga	tagctgtgcc	1500
ggtggtctcy	acaytggttc	caccygcgcg	tcccttagcc	catgcaattg	gggaaggtgt	1560
agactacctg	ctgggcgatg	aggcacaggc	tgcttcagga	actgctcgag	ccgcgtcagg	1620
aaaagcaaga	gctgcctcag	gccgcataag	gcagctract	ctcgccgccc	acaaggggta	1680
cgaggtagtc	gcgaatctrt	tycaggtgcc	ccagaatccy	gtagtcgacg	ggattctygc	1740
ttcacctggg	rtactccgcg	gygcacacaa	cctcgactgc	gtgttragag	agggtgccac	1800
gctattccct	gtggtyatya	cgacagtggg	agaygccatg	acacccaaaag	caytgaacag	1860
caaaatgttt	gctgtcattg	aaggcgtgcg	agaagayctc	caacctccwt	ctcaaagagg	1920
atccttcata	cgaactctct	cyggacayag	agtctatgga	tatgctccag	atgggggtact	1980
tccactggag	actgggagag	aytacaccgt	kgccccata	gatgatgtct	gggacgacag	2040
cattatgctg	tccaaagayc	ccatacctcc	tattgtggga	aacagyggaa	ayctagccat	2100
agcttacatg	gatgtgtttc	gacccaaagt	ccmatccat	gtggcyatga	cgggagccct	2160
caaygcytrt	ggcgagattg	agaamgttag	ctttagaagc	accaagctcg	ccactgcaca	2220
ccgacttggc	ctyaagttgg	ctggtcccg	wgcattygay	gtraacaccg	ggyccaactg	2280
ggcracgtty	atcaaacgtt	tycctcacaa	tccmcgmga	tgggacaggy	tmccytacct	2340
caacctwccm	tayctyccac	cmamwgcwgg	acgycagtwc	sayctkgccm	tggchgchtc	2400
mgagttcaaa	gagaccccmg	aactcgarr	ygcygtsmgw	gcmatggamg	cwgwcwcm	2460
cgtsgaccca	ytrttccrmt	cwgcdctcmr	bgtsttcatg	tggytggaag	araaygggat	2520
tgtracygay	atggcyaaact	tgcmtctcag	cgacccgaac	gcmcaymgga	tgmrraat	2580
ycthgcaay	gcwccmcarg	cmggmagcaa	gtcgcaragr	gccaagtayg	gsacrgcwgg	2640
ctacggagtg	gaggcymgrg	gccccacdcc	agargargca	cagagggara	aagacacacg	2700
gatctcmaag	aagatggara	cbatgggcat	ctacttygca	acaccrgaat	gggtagcact	2760
caaygggcac	cgrgsgccaa	gccccggcca	gctvaagtac	tggcaraaca	camgagaaat	2820
accdgahccm	aacgaggact	aycyagacta	ygtgcaygcr	gagaagagcc	ggttggcrtc	2880
agaagaacar	rtcytaaggg	cagcyacgtc	gatctacggg	gctccaggac	aggcwgarcc	2940
accccaagcy	ttcatagacg	aagtygccar	rgtctatgaa	atcaaccatg	grcgtggycc	3000
maaccargar	cagatgaarg	ayctgctcyt	gactgcgatg	gagatgaagc	atcgcaatcc	3060
caggcgggct	cyaccaaagc	cmaagccaaa	acccaatgct	ccawcacaga	gacccctggg	3120
wcggctgggc	cgctggatca	ggrcbgtctc	tgaygaggac	ytkgagtga	gywcctggga	3180

gtctcccgac accacccgcg caggygtgga caccaattmr kmmhtaswrm atycsaaatt 3240
 ggatccgttc gcgggtcccc 3260

<210> 71

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBV A-segment

<400> 71

```

ggatacgcgc ggtctgaccc cgggggagtc acccggggac aggcgcgtcaa ggtcttggtc 60
caggatggaa ctccctccttc tacaacgcta tcattgatgg tcagtagaga tcagacaaac 120
gatcgcagcg atgacaaaacc tgcaagatca aacccaacag attgttccgt tcatacggag 180
ccttctgatg ccaacaaccg gaccggcgtc cattccggac gacaccctgg agaagcacac 240
tctcaggtca gagacctcga cctacaattt gactgtgggg gacacagggt cagggctaata 300
tgtctttttt cctggattcc ctggctcaat tgtgggtgct cactacacac tgcagagcaa 360
tgggaactac aagttcgatc agatgtctct gactgcccag aacctaccgg ccagttacaa 420
ctactgcagg ctagtgcagc ggagttctac agtgaggcca agcacacttc ctgggtggcg 480
ttatgcacta aacggcacca taaacgccgt gaccttccaa ggaagcctga gtgaactgac 540
agatgttagc tacaatgggt tgatgtctgc aacagccaac atcaacgaca aaattgggaa 600
cgtcctagta ggggaagggg tcaccgtcct cagcttacct acatcatatg atcttgggta 660
tgtgaggcct ggtgacccca ttcccgcaat agggcttgac ccaaaaatgg tagccacatg 720
tgacagcagt gacaggccca gactctacac cataactgca gccgatgatt accaattctc 780
atcacagtac caaccagggt gggtaacaat cacactgttc tcagccaaca ttgatgccat 840
cacaagcttc agcgttgggg gagagctcgt gtttcaaaca agcgtccacg gccttgact 900
gggcgccacc atctacctca taggctttga tgggacagcg gtaatcacca gggctgtggc 960
cgcaacaat gggctgacga ccggcaccga caaccttttg ccattcaatc ttgtgattcc 1020
aacmarcgag ataaccacgc caatcacatc catcaaaact gagatagtga cctccaaaag 1080
tggtggtcag gcaggggatc agatgtcgtg gtcggcaaga gggagcctag cagtgcgat 1140
ccatggtggc aactatccag gggccctccg tcccgtcacg ctagtggcct acgaaagagt 1200
ggcaacagga tccgtcgta cggtcgctgg ggtgagcaac ttcgagctga tcccaaatcc 1260
tgaactagca aagaacctgg ttacagaata cggccgattt gaccaggag ccatgaacta 1320
cacaaaattg atactgagtg agagggacg tcttggcatc aagaccgtct ggccaacaag 1380
ggagtacatg gactttcgtg aatacttcat ggaggtggcc gacctcaact ctcccctgaa 1440
gattgcagga gcattcggct tcaaagacat aatccgggcc ataaggagga tagctgtgcc 1500
ggtggtctcc acattgttcc cacctgccgc tcccctagcc catgcaattg gggaaggtgt 1560
agactacctg ctgggcgatg aggcacaggc tgcttcagga actgctcgag ccgcgtcagg 1620
aaaagcaaga gctgcctcag gccgcataag gcagctgact ctgcgccccg acaaggggta 1680
cgaggtagtc gcgaatctat tccaggtgcc ccagaatccc gtagtcgacg ggattcttgc 1740
ttcacctggg gtactccgcg gtgcacacaa cctcgactgc gtgttaagag agggtgccac 1800
gctattccct gtggttatta cgacagtggg agacgccatg acacccaaag cattgaacag 1860
caaatgttt gctgtcattg aaggcgtgcg agaagacctc caacctcctt ctcaaagagg 1920
atccttcata cgaactctct ctggacacag agtctatgga tatgctccag atgggggtact 1980
tccactggag actgggagag actacaccgt tgtcccaata gatgatgtct gggacgacag 2040
cattatgctg tccaaagatc ccatacctcc tattgtggga aacagtggaa atctagccat 2100
agcttacatg gatgtgtttc gacccaaagt cccaatccat gtggctatga cgggagccct 2160
caatgcttgt ggcgagattg agaaagtaag ctttagaagc accaagctcg ccaactgcaca 2220
ccgacttggc cttaagttgg ctggtcccgg agcattcgat gtaaacaccg ggcccaactg 2280
ggcaacgttc atcaaacgtt tccctcaca tccacgcgac tgggacaggc tcccctacct 2340
caacctacca taccttccac ccaatgcagg acgccagtac caccttgcca tggctgchtc 2400

```

```

agagttcaaa gagacccccg aactcgagag tgccgtcaga gcaatggaag cagcagccaa 2460
cgtggaccca ctattccaat ctgcactcag tgtgttcacg tggctggaag agaattggat 2520
tgtgactgac atggccaact tcgcactcag cgacccgaac gccatcgga tgcgaaattt 2580
tcttgcaaac gcaccacaag caggcagcaa gtcgcaaagg gccagtacg ggacagcagg 2640
ctacggagtg gaggtcggg gccccacacc agaggaagca cagagggaaa aagacacacg 2700
gatctcaaag aagatggaga ccatgggcat ctactttgca acaccagaat gggtagcact 2760
caatgggcac cgaggggcaa gcccggcc gctaaagtac tggcagaaca cacgagaaat 2820
accggaccca aacgaggact atctagacta cgtgcatgca gagaagagcc ggttggcatc 2880
agaagaacaa atcctaaggg cagctacgtc gatctacggg gctccaggac aggcagagcc 2940
acccaagct ttcatagacg aagttgcaa agtctatgaa atcaaccatg gacgtggccc 3000
aaaccaagaa cagatgaaag atctgctctt gactgcatg gagatgaagc atcgcaatcc 3060
caggcgggct ctaccaaagc ccaagccaaa acccaatgct ccaacacaga gacccccctg 3120
tcggctgggc cgctggatca ggaccgtctc tgatgaggac cttgagttag gtacctggga 3180
gtctcccgac accaccgcg caggtgtgga caccaattcg gacttacaac atcccgaatt 3240
ggatccgttc gcgggtcccc                                     3260

```

<210> 72

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence D6948-A of IBV A-segment

<400> 72

```

ggatacgatc ggtctgaccc cgggggagtc acccggggac aggctgacaa ggccttgctc 60
caggatggaa ctctctcttc tacaatgcta tcattgatgg ttagtagaga tcagacaaac 120
gatcgacgag atgacgaacc tgcaagatca aacccaacag attgttccgt tcatacggag 180
ccttctgatg ccaacaaccg gaccggcgtc cattccggac gacaccctag agaagcacac 240
tctcaggtca gagacctcga cctacaattt gactgtgggg gacacagggt cagggttaat 300
tgtctttttc cctggttttc ctggtcfaat tgtgggtgct cactacacac tgcagagcaa 360
tggaactac aagttcgatc agatgtcct gactgccag aacctaccgg ccagctacaa 420
ctactgcagg ctagtgaagc ggagtctcac agtgaggta agcacactcc ctggtggcgt 480
ttatgcacta aatggcacca taaacgcggt gaccttcaa ggaagcctga gtgaactgac 540
agatgttagc tacaatgggt tgatgtctgc aacagccaac atcaacgaca aaatcgggaa 600
cgtcttagta ggggaagggg taacgctctc cagcttacc acatcatatg atcttgggta 660
tgtgagactc ggtgaccca ttcccgctat agggctcgac ccaaaaatgg tagcaacatg 720
tgacagcagt gacaggccca gagtctacac cataactgca gccgatgatt accaattctc 780
atcacagtac caagcagggt gggtaacaat cacactgttc tcagctaata tcgatgccat 840
cacaagcctc agcatcgggg gagaactcgt gtttcaaaca agcgtccaag gccttatact 900
gggtgctacc atctacctta taggctttga tgggactgag gtaatcacca gagctgtggc 960
cgcaracaat gggctaacgg cgggcaactga caaccttatg ccattcaata ttgtgattcc 1020
aaccagcgag ataaccagc caatcacatc catcaaactg gagatagtga cctccaaaag 1080
tggtggtcag gcgggggatc agatgtcatg gtcagcaagt gggagcctag cagtgcgat 1140
ccacggtggc aactatccag gggccctccg tcccgtcaca ctagtagcct acgaaagagt 1200
ggcaacagga tctgtcggtt cggtcgcccg ggtgagcaac ttcgagctga tcccaaatcc 1260
tgaaactagc aagaacctgg tcacagaata cggccgattt gaccaggag ccatgaacta 1320
cacaaaattg atactgagt agagggaccg tcttggcatc aagaccgtat ggccaacaag 1380
ggagtacact gactttcgcg agtacttcat ggaggtggcc gacctcaact ctcccctgaa 1440
gattgcagga gcatttggct tcaaagacat aatccgggcc ctaaggagga tagctgtgcc 1500
ggtggtctct acactgttcc caccgcgcg tccctagacc catgcaattg gggaagggtg 1560
agactacctg ctgggcgatg aggcacaggc tgcttcagga actgctcgag ccgcgtcagg 1620

```

```

aaaagcaaga gctgcctcag gccgcataag gcagctaact ctcgccgccg acaaggggta 1680
cgaggtagtc gcgaatctgt ttcagggtgcc ccagaatcct gtagtcgacg ggattctcgc 1740
ttcacctggg atactccgcg gcgcacacaa cctcgactgc gtgttgagag aggggtgccac 1800
gctattccct gtgggtcatca cgacagtggg agatgccatg acacccaaag cactgaacag 1860
caaaatgttt gctgtcattg aaggcgtgag agaagatctc caacctccat ctcaaagagg 1920
atccttcata cgaactctct ccggacatag agtctatgga tatgctccag atggggtaact 1980
tccactggag actgggagag attacaccgt ggtcccaata gatgatgtct gggacgacag 2040
cattatgctg tccaaagacc ccatacctcc tattgtggga aacagcggaa acctagccat 2100
agcttacatg gatgtgtttc gacccaaagt ccccatccat gtggccatga cgggagccct 2160
caacgcctat ggcgagattg agaacgtgag ctttagaagc accaagctcg ccaactgcaca 2220
ccgacttggc ctcaagttgg ctggtcccgg tgcatttgac gtgaacaccg ggtccaactg 2280
ggcgacgttt atcaaacgtt ttcctcacia tccacgcgac tgggacaggc tcccttacct 2340
caaccttcca taccttccac ccaatgcagg acgccagtac gacctggcca tggccgcttc 2400
agagttcaaa gagacccccg aactcgagag cgccgtcaga gccatggaag cagcagccaa 2460
cgtggacca ctgttccaat ctgcgctcag cgtgttcattg tggctggaag agaatgggat 2520
tgtgactgat atggccaact tcgcactcag cgacccgaac gccatcgga tgcgcaattt 2580
tctcgcaaac gcaccacaag caggcagcaa gtcgcaaaga gccaaagtac ggacagcagg 2640
ctacggagtg gagggccggg gcccactcc agaggaagca cagagggaaa aagacacacg 2700
gatctcaaag aagatggaga ctatgggcat ctactttgca acaccagaat gggtagcact 2760
caatgggcac cgggggccaa gcccggcca gctgaagtac tggcagaaca cagagaaat 2820
acctgatcca aacgaggact acctagacta cgtgcatgca gagaagagcc ggttggcatc 2880
agaagaacaa atcctaaggg cagctacgtc gatctacggg gctccaggac aggcagagcc 2940
acccaagcc ttcatagacg aagtcgcca agtctatgaa atcaaccatg ggcgtggccc 3000
caaccaagaa cagatgaaag atctgctcct gactgcatg gagatgaagc atcgcaatcc 3060
caggcgggct ccaccaaaag ccaagccaaa acccaatgct ccaacacaga gacccctgg 3120
tcggctgggc cgctggatca gggctgtctc tgatgaggac cttgagttag gtacctggga 3180
gtctcccgac accaccgcg cagggtgtgga caccaattcg gccatacaac atcccaaatt 3240
ggatccgttc gcgggtcccc                                     3260

```

<210> 73

<211> 964

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(964)

<223> cDNA sequence TY89-A of IBV A-segment

<400> 73

```

cgtttccctc acaatccccg agactgggac aggttaccct acctcaacct tccctatctt 60
ccaccaacag ctggacgtca gttccatctg gccctggcag cctccgagtt caaagagacc 120
ccagaactcg aagacgtgtg gcgtgcaatg gacgtgctg caaacgtcga cccattgttc 180
cgctcagctc tccaggtctt catgtggttg gaagaaaacg ggattgtaac cgacatggct 240
aacttcgccc tcagcgaccc gaacgcacac aggatgaaaa atttcctagc aaatgctccc 300
caggccggaa gcaagtcgca gagggccaag tatggcacgg ctggctacgg agtggaggct 360
agaggcccca cgccagaaga ggcacagagg gagaaagaca cacggatctc caagaagatg 420
gaaacgatgg gcatctactt cgcaacaccg gaatgggtag cactcaacgg gcaccgaggc 480
ccaagccccg gccagctcaa gtactggcaa aacacaagag aaataccaga acccaacgag 540
gactaccag actatgtgca cgcggagaag agccggttg cgtcagaaga acaggtctta 600
agggcagcca cgtcgatcta cggggctcca ggacaggctg aaccacccca agccttcata 660
gacgaagtgc ccagggtcta tgaaatcaac catgggcgtg gtccaaacca ggagcagatg 720
aaggacctgc tctgactgc gatggagatg aagcatcgca atcccaggcg ggctccacca 780
aagccaaagc caaaacccaa tgctccatca cagagacccc ctggacggct gggccgctgg 840

```

```

atcaggacgg tctctgacga ggacttggag tgaggctcct gggagtctcc cgacaccacc 900
cgcgcagggtg tggacaccaa ttaatcacta gtgaattcga aattggatcc gttcgcgggt 960
cccc                                              964

```

<210> 74

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> Consensus cDNA sequence of IBV B-segment

<400> 74

```

ggatacgatg ggtctgaccc tctgggagtc acgaattaac gtggctacta ggggygattrm 60
ccrccgctrg ctgccacgtt agtggctcct cttcttgatg attctrccac catgagtgc 120
rttttcaaya gtccacaggc gcgaagcamg atmtcagcag cgttcggcat aaagcctacw 180
gctggacarg aygtggaaga actcytgatc cctaargtyt gggtgccacc tgaggatccs 240
ytkgccagcc ctagtcgwct ggcmaagttc ctcagrgara acggctacaa rrttytgag 300
ccacggtctc trccygagaa tgaggagtat gagaccgayc aaatactccc wgacytagcw 360
tggatgmgrc agatagargg rgctgtttta aaaccmacyc tatctctccc yattggagay 420
caggagtact tcccwaarta ctacccaaca caycgcccka gcaaggaraa gccaatgcg 480
taccgcccmg ayatcgcayt actcaagcag atgatyacyt tgtttctcca ggttccmgag 540
gccammgakr rcctwaarga tgargtmacc ctmytracc aaacatwag rgayaargcc 600
tayggragtg ggacctacat gggacargcm acymgacttg tkgcyatgaa rgaggtygcc 660
actggragaa acccaacaa rgatcctcta aagcttgggt acacytttga gagcatmgcs 720
cagctacttg acatcacwyt accggtaggc ccaccgggtg aggatgacaa gccctgggtr 780
ccactcacia grgtgccgtc amggatggtg gtwctgacgg gmgacgtaga tggsgamttt 840
gaggttgarg aytaccttcc caaaatcaac ctcaagtcac caagtggact rccmtatgtw 900
ggtcgcacca aaggagarac wattggsgag atgatagcya tmtcraacca gtttctymga 960
gagctatcar crctgytgaa gcarggtgca gggacaaarg ggtcraacaa gaagaagctr 1020
ctcagcatgy taagtgcata ytggtactta tcatgygggc ttttgtttcc maaggctgar 1080
aggtacgaca aaagyacatg gctcaccaag acccgkaaca tatggtcagc tccatcmcca 1140
acacacctca tgatctcwat gatmacctgg cccgtgatgt ccaayagccc aaayaacgtg 1200
ttgaacattg argggtgtcc rtcactctac aarttcaacc cgtyagagg wgggytraac 1260
aggatcgtsg agtgatawt ggcycggaw gaaccaagg cyytwgtata tgckgacaac 1320
atatacatgt tycactcmaa cacgtggtac tcaattgacc tagagaaggg tgaggcaaac 1380
tgackcgty aacacatgca rgccgcmatg tactacatmc tyaccagagg rtggtcmgay 1440
aacggygacc cmatgttcaa tcaracatgg gccaccttg csatgaacat tgccccwgct 1500
ctagtkgttg actcatcrtg yctgatwatg aacctkcar tyaagacmta tgggtcaaggc 1560
agygggaatg cagccacstt catcaacaac cayctyytka gcacsctwgt gctwgaccag 1620
tggaacytga tgarrcarcc yagwccagac agcgargagt tcaartcaat tgargacaag 1680
ctrngyatca acttyaagat tgagaggtcc attgatgaya tyaggggcaa gctsagacag 1740
cttgctccyc ttgcacaacc aggttacctg agtggrgggg tygaaccaga rcaayccagc 1800
ccaactgtwg agctkgacct actmggrtg twcgcwacwt acagcaaaga tctygggatc 1860
tatgtgccgg tgcttgacaa ggaacgcyta ttttgytctg ctgcgtatcc caarggrgta 1920
gagaayaara gyctcaartc caargtyggg atcgagcarg catacaargt wgtcaggatay 1980
gaggcggttg gggttgtagg tggttggaac taccactcc tgaacaaagc ytgcaagaay 2040
aaygcargyg cmgctcggcg gcatctggag gccaaagggg tcccrctcga ygagttcctm 2100
gccgagtggt cwgagytgtc mgagttcggw gargcyttcg aaggcttcaa yatcaagctg 2160
acmgtaacay ckagagacct mgccgaactk aacarrccag tccccccaa rccyccaaat 2220
gtcaacagac cagtcaacac yggkggrctm aaggcagtc gcaaygccct caagaccggy 2280
cggtayagra aygaagccgg actragtggy ctgctctyc tagccacmgc mmgmagccgw 2340

```

ctrcargayg	cagtyaaggc	caaggcagar	gccgagaaac	tccacaagtc	yaagccmgay	2400
gaccccgatg	cagactgggt	ygaamgrtca	gaaacyctgt	cagacctkct	ggagaaagcc	2460
gacatygcc	gcaaggtcgc	ycactcagca	ctcgtggaaa	caagcgacgc	ycttgaagcr	2520
gtycagtcra	cytcmgtgta	cacyccmaag	taccagarg	tyaagaaccc	acagaccgcc	2580
tccaaccccg	ttgttgggct	ccacctgccc	gccaagarg	ccaccggtgt	ccaggcmgct	2640
cttctcggag	caggracgag	cagaccaatg	gggatggagg	cyccaacacg	gtccaagaac	2700
gccgtgaaaa	tggccaaamg	gcggcaacgc	caaaargaga	gccgccaaya	gccatgatgg	2760
gaaccactca	agaagaggac	actaayccca	gaccccgat	ccccggcctt	cgctgcggg	2820
ggcccc						2827

<210> 75

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> cDNA sequence CEF94-B of IBV B-segment

<400> 75

ggatacgatg	ggtctgacct	tctgggagtc	acgaattaac	gtggctacta	ggggcgataa	60
ccgccgctgg	ctgccacgtt	agtggctcct	cttcttgatg	attctgccac	catgagtgc	120
atthttcaaca	gtccacaggc	gcgaagcacg	atctcagcag	cgttcggcat	aaagcctact	180
gctggacaag	acgtggaaga	actcttgatc	cctaaagttt	gggtgccacc	tgaggatccg	240
cttgccagcc	ctagtgcact	ggcaaagtcc	ctcagagaga	acggctacaa	agttytgacg	300
ccacggtctc	tgcccagaga	tgaggagtat	gagaccgacc	aaatactccc	agacttagca	360
tggatgcgac	agatagaagg	ggctgtttta	aaaccactc	tatctctccc	tattggagat	420
caggagtact	tcccaaagta	ctacccaaca	catcgcccta	gcaaggagaa	gccaatgcg	480
taccgcgag	acatgcgact	actcaagcag	atgatttacc	tgtttctcca	ggttccagag	540
gccaacgagg	gcctaaagga	tgaagtaacc	ctcttgacct	aaaacataag	ggacaaggcc	600
tatggaagtg	ggacctacat	gggacaagca	actcgacttg	tggccatgaa	ggaggtcgcc	660
actggaagaa	acccaaacaa	ggatcctcta	aagcttgggt	acacttttga	gagcatcgcg	720
cagctacttg	acatcacact	accggtaggc	ccaccggtg	aggatgacaa	gccctgggtg	780
ccactcaca	gagtgcgctc	acggatggtg	gtactgacgg	gagacgtaga	tggcgacttt	840
gaggttgaag	attaccttcc	caaaatcaac	ctcaagtcat	caagtggact	accatatgta	900
ggtcgaccca	aaggagagac	aattggcgag	atgatagcta	tctcaaacca	gtttctcaga	960
gagctatcaa	cactgttgaa	gcaagggtgca	gggacaaagg	ggtcaaacaa	gaagaagcta	1020
ctcagcatgt	taagtgcact	ttggtaacta	tcatgcgggc	ttttgtttcc	aaaggctgaa	1080
aggtacgaca	aaagtacatg	gctcaccaag	acccggaaca	tatggtcagc	tccatcccca	1140
acacacctca	tgatctctat	gatcacctgg	cccgtgatgt	ccaacagccc	aaataacgtg	1200
ttgaacattg	aagggtgtcc	atcactctac	aaattcaacc	cgttcagagg	agggttgaac	1260
aggatcgctg	agtggatatt	ggccccggaa	gaaccaagg	ctcttgata	tgccgacaac	1320
atatacattg	tyactcaaaa	cacgtggtac	tcaattgacc	tagagaaggg	tgaggcaaac	1380
tgactcgcc	aacacatgca	agccgcaatg	tactacatac	tcaccagagg	gtggtcagac	1440
aacggcgacc	caatgttcaa	tcaaacatgg	gccacctttg	ccatgaacat	tgcccctgct	1500
ctagtgggtg	actcatcggt	cctgataatg	aacctgcaaa	ttaagacct	tggtaaggc	1560
agcgggaatg	cagccacgtt	catcaacaac	cacctcttga	gcacgctagt	gcttgaccag	1620
tggaacctga	tgagacagcc	cagaccagac	agcgaggagt	tcaaatcaat	tgaggacaag	1680
ctaggtatca	actttaagat	tgagagggtc	attgatgata	tcaggggcaa	gctgagacag	1740
cttgtcctcc	ttgcacaacc	agggtacctg	agtggggggg	ttgaaccaga	acaatccagc	1800
ccaactgttg	agcttgacct	actagggtgg	tcagctacat	acagcaaaga	tctcgggatc	1860
tatgtgccgg	tgcttgacaa	ggaacgccta	ttttgttctg	ctgcgtatcc	caaggagata	1920
gagaacaaga	gtctcaagtc	caaagtcggg	atcgagcagg	catacaaggt	agtcagggtat	1980

gaggcggttga	ggttggttagg	tggttgggaac	taccactcc	tgaacaaagc	ctgcaagaat	2040
aatgcagggc	ccgctcggcg	gcatctggag	gccaaggggt	tcccactcga	cgagttccta	2100
gccgagtgg	ctgagctgtc	agagttcgg	gaggccttcg	aaggcttcaa	tatcaagctg	2160
accgtaacat	ctgagagcct	agccgaactg	aacaagccag	taccccccaa	gcccccaa	2220
gtcaacagac	cagtcaacac	tgggggactc	aaggcagtc	gcaacgccct	caagaccggt	2280
cggtagacga	acgaagccgg	actgagtggt	ctcgtccttc	tagccacagc	aagaagccgt	2340
ctgcaagatg	cagttaaggc	caaggcagaa	gccgagaaac	tccacaagtc	caagccagac	2400
gaccccgatg	cagactgggt	cgaaagatca	gaaactctgt	cagaccttct	ggagaaagcc	2460
gacatcgcca	gcaaggctgc	ccactcagca	ctcgtggaaa	caagcgacgc	ccttgaagca	2520
gttcagtcga	cttccgtgta	cactcccaag	taccagaag	tcaagaaccc	acagaccgcc	2580
tccaaccccg	ttgttgggct	ccacctgccc	gccaagagag	ccaccggtgt	ccaggccgct	2640
cttctcggag	caggaaacgag	cagaccaatg	gggatggagg	ccccaacacg	gtccaagaac	2700
gccgtgaaaa	tggccaaacg	gcggcaacgc	caaaaggaga	gccgccaaca	gccatgatgg	2760
gaaccactca	agaagaggac	actaatccca	gaccccgat	ccccggcctt	cgctgcggg	2820
ggcccc						2827

<210> 76

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> cDNA sequence D6948-B of IBV B-segment

<400> 76

ggatacga	ggtctgaccc	tctgggagtc	acgaattaac	gtggctacta	ggggtgatgc	60
ccaccgctag	ctgccacgtt	agtggctcct	cttcttgatg	attctaccac	catgagtgc	120
gttttcaata	gtccacaggc	gcgaagcaag	atatcagcag	cgttcggcat	aaagcctaca	180
gctggacagg	atgtggaaga	actcctgatc	cctaaggctc	gggtgccacc	tgaggatccc	240
ttggccagcc	ctagtcgtct	ggccaagttc	ctcagggaaa	acggctacaa	gattctgcag	300
ccacggtctc	tacctgagaa	tgaggagtat	gagaccgatc	aaatactccc	tgacctagct	360
tggatgaggc	agatagaggg	agctgtttta	aaaccaaccc	tatctctccc	cattggagac	420
caggagtact	tccctaata	ctaccaaca	caccgcccga	gcaaggaaaa	gccaatgcg	480
taccgcccc	atatcgcat	actcaagcag	atgatctact	tgtttctcca	ggttcccag	540
gccacagata	accttaaaga	tgaggtcacc	ctactaacc	aaaacattag	agataaagcc	600
tacgggagtg	ggacctacat	gggacaggcc	accagacttg	ttgctatgaa	agaggttgcc	660
actgggagaa	acccaaacaa	agatcctcta	aagcttgggt	acaccttga	gagcatagcc	720
cagctacttg	acatcacttt	accggtaggc	ccaccggtg	aggatgacaa	gccctgggta	780
ccactcacia	gggtgccgtc	aaggatgttg	gttctgacgg	gcgacgtaga	tggggaattt	840
gaggttgagg	actaccttcc	caaaatcaac	ctcaagtc	caagtggact	gccctatgtt	900
ggtcgcacca	aaggagaaac	tattggggag	atgatagcca	tatcgaacca	gtttcttcga	960
gagctatcag	cgctgctgaa	gcagggtgca	gggacaaaag	ggtcgaacaa	gaagaagctg	1020
ctcagcatgc	taagtgacta	ctggtactta	tcatgtgggc	ttttgtttcc	caaggctgag	1080
aggtacgaca	aaagcacatg	gctcaccaag	acccgtaaca	tatggtcagc	tccatcacca	1140
acacacctca	tgatctcaat	gataacctgg	cccgtgatgt	ccaatagccc	aaacaacgtg	1200
ttgaacattg	aggggtgtcc	gtcactctac	aagttcaacc	cgttttagagg	tgggctaaac	1260
aggatcgtgg	agtggataat	ggctccggat	gaaccaag	ccttagtata	tgctgacaac	1320
atatacattg	ttcactccaa	cacgtggtac	tcaattgacc	tagagaagg	tgaggcaaac	1380
tgcacgcgtc	aacacatgca	ggccgccatg	tactacatcc	ttaccagagg	atggtccgat	1440
aacggtgacc	ccatgttcaa	tcagacatgg	gccacctttg	cgatgaacat	tgccccagct	1500
ctagttgtgg	actcatcatg	tctgattatg	aaccttcaga	tcaagacata	tggtcaaggc	1560
agtgggaatg	cagccacctt	catcaacaac	catcttctta	gcacccttgt	gctagaccag	1620

```

tgggaacttga tgaagcaacc tagtccagac agcgaagagt tcaagtcaat tgaagacaag 1680
ctgggcatca acttcaagat tgagaggtcc attgatgaca ttaggggcaa gctcagacag 1740
cttgtcccc ttgcacaacc agggtagctg agtggagggg tcgaaccaga gcaacccagc 1800
ccaactgtag agctggacct actcggatgg tctgcaactt acagcaaaga tcttgggata 1860
tatgtgccgg tgcttgacaa ggaacgctta ttttgctctg ctgcgatatcc caaaggggta 1920
gagaataaaa gcctcaaata caaggttggg atcgagcaag catacaaagt tgtcaggtag 1980
gaggcggttg gggttggtagg tggttggaac taccactcc tgaacaaagc ttgcaagaac 2040
aatgcaagtg cagctcggcg gcatctggag gccaaggggt tcccgctcga tgagttcctc 2100
gccgagtggg cagagttgtc cgagttcgga gaagctttcg aaggcttcaa catcaagctg 2160
acagtaacac cggagagcct cgccgaactt aacagaccag tccccccaa acctccaaat 2220
gtcaacagac cagtcaacac cggtgaggta aaggcagtc gcaatgccct caagaccggc 2280
cggtatagaa atgaagccgg actaagtggc ctcgtcctcc tagccaccgc ccgcagccga 2340
ctacaggacg cagtcaaggc caaggcagag gccgagaaac tccacaagtc taagcccgat 2400
gaccccgatg cagactgggt tgaacgggtc gaaaccctgt cagacctgct ggagaaagcc 2460
gacattgcca gcaaggctgc tcaactcagca ctcgtggaaa caagcgacgc tcttgaagcg 2520
gtccagtcaa cctcagtgta cccccaaaag taccagagg ttaagaaccc acagaccgcc 2580
tccaaccccg ttgttgggct ccacctgccc gccaaagagg ccaccggtgt ccaggcagct 2640
cttctcggag cagggacgag cagaccaatg gggatggagg ctccaacacg gtccaagaac 2700
gccgtgaaaa tggccaaaag gcggcaacgc caaaaagaga gccgccaata gccatgatgg 2760
gaaccactca agaagaggac actaacccca gaccccgat ccccggcctt cgcctgcggg 2820
ggcccc

```

```

<210> 77
<211> 1012
<212> PRT
<213> Infectious bursal disease virus

```

```

<220>
<221> DOMAIN
<222> (1)..(1012)
<223> Consensus sequence of IBDV polyprotein

```

```

<220>
<221> MISC_FEATURE
<222> (222)
<223> The 'Xaa' at position 222 may be any amino acid

```

```

<220>
<221> MISC_FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

```

```

<220>
<221> MISC_FEATURE
<222> (253)
<223> The 'Xaa' at position 253 may be any amino acid

```

```

<220>
<221> MISC_FEATURE
<222> (256)
<223> The 'Xaa' at position 256 may be any amino acid

```

```

<220>

```

```

<221> MISC_FEATURE
<222> (279)
<223> The 'Xaa' at position 279 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (284)
<223> The 'Xaa' at position 284 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (290)
<223> The 'Xaa' at position 290 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (294)
<223> The 'Xaa' at position 294 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (299)
<223> The 'Xaa' at position 299 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (330)
<223> The 'Xaa' at position 330 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (451)
<223> The 'Xaa' at position 451 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (541)
<223> The 'Xaa' at position 541 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (680)
<223> The 'Xaa' at position 680 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (685)
<223> The 'Xaa' at position 685 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (715)
<223> The 'Xaa' at position 715 may be any amino acid

<400> 77

```


Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
 85 90 95
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
 100 105 110
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
 115 120 125
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
 130 135 140
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
 145 150 155 160
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
 165 170 175
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
 180 185 190
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Xaa Gly Gly
 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
 225 230 235 240
 Ser Xaa Gly Gly Glu Leu Val Phe Gln Thr Ser Val Xaa Gly Leu Xaa
 245 250 255
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
 260 265 270
 Thr Arg Ala Val Ala Ala Xaa Asn Gly Leu Thr Xaa Gly Thr Asp Asn
 275 280 285
 Leu Xaa Pro Phe Asn Xaa Val Ile Pro Thr Xaa Glu Ile Thr Gln Pro

290	295	300
Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln 305 310 315 320		
Ala Gly Asp Gln Met Ser Trp Ser Ala Xaa Gly Ser Leu Ala Val Thr 325 330 335		
Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val 340 345 350		
Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val 355 360 365		
Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val 370 375 380		
Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu 385 390 395 400		
Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr 405 410 415		
Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu 420 425 430		
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile 435 440 445		
Arg Ala Xaa Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro 450 455 460		
Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu 465 470 475 480		
Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser 485 490 495		
Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala 500 505 510		
Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln 515 520 525		
Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly 530 535 540		
Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro 545 550 555 560		
Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn 565 570 575		
Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro 580 585 590		

Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Xaa Gly Glu Ile Glu Xaa Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880

Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
 965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
 980 985 990
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp
 995 1000 1005
 Glu Asp Leu Glu
 1010

<210> 78
 <211> 1012
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(1012)
 <223> Sequence of IBDV polyprotein CEF94-PP

<400> 78
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr

85										90					95															
Asn	Tyr	Cys	Arg	Leu	Val	Ser	Arg	Ser	Leu	Thr	Val	Arg	Ser	Ser	Thr															
			100						105					110																
Leu	Pro	Gly	Gly	Val	Tyr	Ala	Leu	Asn	Gly	Thr	Ile	Asn	Ala	Val	Thr															
		115						120					125																	
Phe	Gln	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Val	Ser	Tyr	Asn	Gly	Leu															
	130						135					140																		
Met	Ser	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	Val	Leu	Val															
145						150				155					160															
Gly	Glu	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro	Thr	Ser	Tyr	Asp	Leu	Gly															
				165					170					175																
Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	Asp	Pro	Lys															
			180					185					190																	
Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	Tyr	Thr	Ile															
		195					200					205																		
Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	Pro	Gly	Gly															
	210						215					220																		
Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu															
225						230				235					240															
Ser	Val	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	His	Gly	Leu	Val															
				245					250					255																
Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Ala	Val	Ile															
			260					265					270																	
Thr	Arg	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu	Thr	Thr	Gly	Thr	Asp	Asn															
		275					280					285																		
Leu	Leu	Pro	Phe	Asn	Leu	Val	Ile	Pro	Thr	Asn	Glu	Ile	Thr	Gln	Pro															
	290					295					300																			
Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	Gly	Gly	Gln															
305					310					315					320															
Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Arg	Gly	Ser	Leu	Ala	Val	Thr															
				325					330					335																
Ile	His	Gly	Gly	Asn	Tyr	Pro	Gly	Ala	Leu	Arg	Pro	Val	Thr	Leu	Val															
			340					345					350																	
Ala	Tyr	Glu	Arg	Val	Ala	Thr	Gly	Ser	Val	Val	Thr	Val	Ala	Gly	Val															
		355					360					365																		
Ser	Asn	Phe	Glu	Leu	Ile	Pro	Asn	Pro	Glu	Leu	Ala	Lys	Asn	Leu	Val															
	370					375					380																			

Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670

Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn

[illegible]

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
 180 185 190
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly
 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
 225 230 235 240
 Ser Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile
 245 250 255
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
 260 265 270
 Thr Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn
 275 280 285
 Leu Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro
 290 295 300
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
 305 310 315 320
 Ala Gly Asp Gln Met Ser Trp Ser Ala Ser Gly Ser Leu Ala Val Thr
 325 330 335
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
 340 345 350
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460

Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Ile Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Tyr Gly Glu Ile Glu Asn Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Ser Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr Asp Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala

755					760					765					
Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser
770					775					780					
Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp
785					790					795					800
Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn
				805					810					815	
Phe	Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	Arg	Ala	Lys
			820					825					830		
Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	Thr	Pro	Glu
		835					840					845			
Glu	Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	Met	Glu	Thr
	850					855					860				
Met	Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	Asn	Gly	His
865					870					875					880
Arg	Gly	Pro	Ser	Pro	Gly	Gln	Leu	Lys	Tyr	Trp	Gln	Asn	Thr	Arg	Glu
				885					890					895	
Ile	Pro	Asp	Pro	Asn	Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	Ala	Glu	Lys
			900					905					910		
Ser	Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	Thr	Ser	Ile
		915					920					925			
Tyr	Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	Ile	Asp	Glu
	930					935					940				
Val	Ala	Lys	Val	Tyr	Glu	Ile	Asn	His	Gly	Arg	Gly	Pro	Asn	Gln	Glu
945					950					955					960
Gln	Met	Lys	Asp	Leu	Leu	Leu	Thr	Ala	Met	Glu	Met	Lys	His	Arg	Asn
				965					970					975	
Pro	Arg	Arg	Ala	Pro	Pro	Lys	Pro	Lys	Pro	Lys	Pro	Asn	Ala	Pro	Thr
			980				985						990		
Gln	Arg	Pro	Pro	Gly	Arg	Leu	Gly	Arg	Trp	Ile	Arg	Ala	Val	Ser	Asp
		995				1000					1005				
Glu	Asp	Leu	Glu												
	1010														

<210> 80

<211> 290

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(290)

<223> Sequence of IBDV polyprotein TY89-PP

<400> 80

Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn
1 5 10 15

Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu
20 25 30

Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg
35 40 45

Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu
50 55 60

Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala
65 70 75 80

Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu
85 90 95

Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly
100 105 110

Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala
115 120 125

Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly
130 135 140

Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly
145 150 155 160

Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro
165 170 175

Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg
180 185 190

Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly
195 200 205

Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala
210 215 220

Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met
225 230 235 240

Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg
245 250 255

Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg
260 265 270

Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp
275 280 285

Leu Glu
290

<210> 81
<211> 881
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(881)
<223> Consensus sequence of IBDV VP1

<220>
<221> MISC_FEATURE
<222> (4)
<223> The 'Xaa' at position 4 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (13)
<223> The 'Xaa' at position 13 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (61)
<223> The 'Xaa' at position 61 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (145). . . (147)
<223> The 'Xaa' at positions 145-147 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (287)
<223> The 'Xaa' at position 287 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (390)
<223> The 'Xaa' at position 390 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (393)
 <223> The 'Xaa' at position 393 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (508)
 <223> The 'Xaa' at position 508 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (511)
 <223> The 'Xaa' at position 511 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (546)
 <223> The 'Xaa' at position 546 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (562)
 <223> The 'Xaa' at position 562 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (646)
 <223> The 'Xaa' at position 646 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (687)
 <223> The 'Xaa' at position 687 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (695)
 <223> The 'Xaa' at position 695 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (880) . . . (881)
 <223> The 'Xaa' at positions 880-881 may be any amino acid

<400> 81
 Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala
 1 5 10 15

 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30

 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser

35					40					45					
Arg	Leu	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Xaa	Leu	Gln	Pro
50						55					60				
Arg	Ser	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro
65					70					75					80
Asp	Leu	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr
				85					90					95	
Leu	Ser	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro
			100					105					110		
Thr	His	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile
		115					120					125			
Ala	Leu	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala
	130					135					140				
Xaa	Xaa	Xaa	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg
145					150					155					160
Asp	Lys	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu
				165					170					175	
Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro
			180					185					190		
Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile
	195						200					205			
Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro
	210					215					220				
Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp
225					230					235					240
Gly	Xaa	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser
			245						250					255	
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly
			260					265					270		
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Xaa	Leu
	275						280					285			
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu
	290					295					300				
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro
305					310					315					320
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn
				325					330					335	

Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
 340 345 350
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
 355 360 365
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
 370 375 380
 Ile Val Glu Trp Ile Xaa Ala Pro Xaa Glu Pro Lys Ala Leu Val Tyr
 385 390 395 400
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
 405 410 415
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
 420 425 430
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
 435 440 445
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
 450 455 460
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
 465 470 475 480
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
 485 490 495
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Xaa Gln Pro Xaa Pro
 500 505 510
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
 515 520 525
 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
 530 535 540
 Val Xaa Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560
 Gln Xaa Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa
 865 870 875 880

Xaa

<210> 82
 <211> 881
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(881)

<223> Sequence of IBDV CEF94-VP1

<400> 82

Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
130 135 140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
225 230 235 240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser

245																250																255															
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly																																
			260				265						270																																		
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu																																
			275				280						285																																		
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu																																
			290				295						300																																		
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro																																
305						310						315			320																																
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn																																
						325						330			335																																
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr																																
						340						350																																			
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly																																
						355						365																																			
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg																																
						375						380																																			
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr																																
385						390						395			400																																
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp																																
						405						410			415																																
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala																																
						420						430																																			
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met																																
						435						445																																			
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu																																
						450						460																																			
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr																																
465						470						475			480																																
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu																																
						485						490			495																																
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro																																
						500						510																																			
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe																																
						515						525																																			
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu																																
						530						540																																			
						535						545																																			

Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575

Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590

Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640

Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655

Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670

Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
 675 680 685

Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700

Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720

Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735

Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765

Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800

Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815

Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830

Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
835 840 845

Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
850 855 860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln
865 870 875 880

Pro

<210> 83

<211> 879

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(879)

<223> Sequence of IBV D6948-VP1

<400> 83

Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
130 135 140

Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu

				165				170				175			
Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro
			180					185					190		
Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile
			195					200					205		
Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro
			210					215					220		
Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp
			225					230					235		
Gly	Glu	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser
			245					250					255		
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly
			260					265					270		
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Ala	Leu
			275					280					285		
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu
			290					295					300		
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro
			305					310					315		
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn
			325					330					335		
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr
			340					345					350		
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly
			355					360					365		
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg
			370					375					380		
Ile	Val	Glu	Trp	Ile	Met	Ala	Pro	Asp	Glu	Pro	Lys	Ala	Leu	Val	Tyr
			385					390					395		
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp
			405					410					415		
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala
			420					425					430		
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met
			435					440					445		
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu
			450					455					460		

Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	465	470	475	480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	485	490	495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Lys	Gln	Pro	Ser	Pro	500	505	510	
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	515	520	525	
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	530	535	540	
Val	Pro	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	545	550	555	560
Gln	Pro	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	565	570	575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	580	585	590	
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	595	600	605	
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	610	615	620	
Ala	Leu	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	625	630	635	640
Cys	Lys	Asn	Asn	Ala	Ser	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	645	650	655	
Phe	Pro	Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	660	665	670	
Gly	Glu	Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Pro	Glu	675	680	685	
Ser	Leu	Ala	Glu	Leu	Asn	Arg	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	690	695	700	
Asn	Arg	Pro	Val	Asn	Thr	Gly	Gly	Leu	Lys	Ala	Val	Ser	Asn	Ala	Leu	705	710	715	720
Lys	Thr	Gly	Arg	Tyr	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Gly	Leu	Val	Leu	725	730	735	
Leu	Ala	Thr	Ala	Arg	Ser	Arg	Leu	Gln	Asp	Ala	Val	Lys	Ala	Lys	Ala	740	745	750	

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln
 865 870 875

<210> 84
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Consensus sequence of IBDV VP5

<220>
 <221> MISC_FEATURE
 <222> (14)
 <223> The 'Xaa' at position 14 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (45)
 <223> The 'Xaa' at position 45 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (74)
 <223> The 'Xaa' at position 74 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (125)
 <223> The 'Xaa' at position 125 may be any amino acid

<220>

<221> MISC_FEATURE

<222> (133)

<223> The 'Xaa' at position 133 may be any amino acid

<400> 84

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His
35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly
65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg
115 120 125

Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
130 135 140

Glu
145

<210> 85

<211> 145

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(145)

<223> Sequence of IBDV D6948-VP5

<400> 85

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala

Asn	Asn	Arg	Thr	Gly	Val	His	Ser	Gly	Arg	His	Pro	Arg	Glu	Ala	His
	35						40					45			
Ser	Gln	Val	Arg	Asp	Leu	Asp	Leu	Gln	Phe	Asp	Cys	Gly	Gly	His	Arg
	50					55					60				
Val	Arg	Ala	Asn	Cys	Leu	Phe	Pro	Trp	Phe	Pro	Trp	Leu	Asn	Cys	Gly
	65				70				75						80
Cys	Ser	Leu	His	Thr	Ala	Glu	Gln	Trp	Glu	Leu	Gln	Val	Arg	Ser	Asp
			85					90						95	
Ala	Pro	Asp	Cys	Pro	Glu	Pro	Thr	Gly	Gln	Leu	Gln	Leu	Leu	Gln	Ala
		100						105					110		
Ser	Glu	Ser	Glu	Ser	His	Ser	Glu	Val	Lys	His	Thr	Pro	Trp	Trp	Arg
	115						120					125			
Leu	Cys	Thr	Lys	Trp	His	His	Lys	Arg	Arg	Asp	Leu	Pro	Arg	Lys	Pro
	130					135					140				
Glu															
145															

<210> 86
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBVD CEF94-VP5

Met	Val	Ser	Arg	Asp	Gln	Thr	Asn	Asp	Arg	Ser	Asp	Asp	Lys	Pro	Ala
1				5					10					15	
Arg	Ser	Asn	Pro	Thr	Asp	Cys	Ser	Val	His	Thr	Glu	Pro	Ser	Asp	Ala
			20					25					30		
Asn	Asn	Arg	Thr	Gly	Val	His	Ser	Gly	Arg	His	Pro	Gly	Glu	Ala	His
	35						40					45			
Ser	Gln	Val	Arg	Asp	Leu	Asp	Leu	Gln	Phe	Asp	Cys	Gly	Gly	His	Arg
	50					55					60				
Val	Arg	Ala	Asn	Cys	Leu	Phe	Pro	Trp	Ile	Pro	Trp	Leu	Asn	Cys	Gly
	65				70				75						80
Cys	Ser	Leu	His	Thr	Ala	Glu	Gln	Trp	Glu	Leu	Gln	Val	Arg	Ser	Asp
				85				90						95	

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
 115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140

Glu
 145

<210> 87

<211> 149

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(149)

<223> Sequence of IBDV D6948-VP5

<400> 87

Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp
 1 5 10 15

Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu
 20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro
 35 40 45

Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys
 50 55 60

Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp
 65 70 75 80

Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln
 85 90 95

Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln
 100 105 110

Leu Leu Gln Ala Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr
 115 120 125

Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu
 130 135 140

Pro Arg Lys Pro Glu
 145